OIPE

RAW SEQUENCE LISTING   DATE: 06/07/2001
PATENT APPLICATION: US/09/762,230   TIME: 11:27:38

Input Set : **A:\FUJII Sequence listing.txt**
Output Set: **C:\CRF3\06072001\I762230.raw**

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 3 <110> APPLICANT: FUJII, Tadashi
 4        NARITA, Takao
 5        NAKATA, Kuniho
 6        AGEMATU, Hitosi
 7        TSUNEKAWA, Hiroshi
 8        ISSHIKI, Kunio
 9        YOSHIOKA, Takeo
11 <120> TITLE OF INVENTION: Gene participating in the production of homoglutamic
12        acid and its use
14 <130> FILE REFERENCE: 2001-0116A/LC/00202
16 <140> CURRENT APPLICATION NUMBER: 09/762,230
17 <141> CURRENT FILING DATE: 2001-05-25
19 <150> PRIOR APPLICATION NUMBER: JP10/232382
20 <151> PRIOR FILING DATE: 1998-08-05
22 <150> PRIOR APPLICATION NUMBER: JP11/182362
23 <151> PRIOR FILING DATE: 1999-06-28
25 <160> NUMBER OF SEQ ID NOS: 9
27 <170> SOFTWARE: PatentIn Ver. 2.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 2663
31 <212> TYPE: DNA
32 <213> ORGANISM: Flavobacterium lutescens
34 <220> FEATURE:
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36 <222> LOCATION: (801)..(2276)
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43 gctccggcag cggcgcctgg gcaatcagtt cgggaggcag gtggtaggca aaatcggact 180
45 tcttcaacgc cggcagctcg atacaacggg ggcgtcagtt tacgcccctg taccgcctgt 240
47 gccctcaccg ctcgaacttg gtgcccagga tcaccgccgt ggtggtgcgc tcgaccccat 300
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51 tcgccaccag gtcatgcgcg ccactgaccg aatgcaggct gcgcaccgca gcaatggcct 420
53 gcagcgcccg cacgaccgcc ggcattttct tcggcatcac ggtgatggag atatgcgcgc 480
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57 tgtgctgcag ccgctcgatc cggctctgca ccgtggtccg cgacaccccg agccggcgcg 600
59 ccagcgccgc ggtcgaggcg cgcgcatcct cacgcaacag gtcaagcaac tgtgcatccg 660
61 cctgggaaat ggtcactttg tcgaaaacct tcgtcaatc cgccgaaacc ggccattgat 720
63 ttgagcagat tcgcactgcc atttgtagtg cgttaacggt tacaactaac actagacaca 780
65 atcagcacgg attcagcatg tcc ctt ctt gcc ccg ctc gcc ccg ctc cgc gcc 833
66                     Ser Leu Leu Ala Pro Leu Ala Pro Leu Arg Ala
67                      1               5                  10
69 cat gcc ggc acc cgc ctt acc cag ggc ctg tct gac ccg cag gtc gag     881
70 His Ala Gly Thr Arg Leu Thr Gln Gly Leu Ser Asp Pro Gln Val Glu
71              15                  20                  25
73 cag ctg gcc gcc aac cac cct gac ctg cgc gcc gcc atc gac gcc gct     929
74 Gln Leu Ala Ala Asn His Pro Asp Leu Arg Ala Ala Ile Asp Ala Ala
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75          30                    35                    40
77  gcc gac gaa tac gcg cgc atc aaa ccg cag gcc gcg gca ttg ctg gac    977
78  Ala Asp Glu Tyr Ala Arg Ile Lys Pro Gln Ala Ala Ala Leu Leu Asp
79          45                    50                    55
81  ctg gat gaa agc gcg cag atc gcc gcc gtg cag gat ggc ttc gtc aac   1025
82  Leu Asp Glu Ser Ala Gln Ile Ala Ala Val Gln Asp Gly Phe Val Asn
83  60                    65                    70                    75
85  ttc tat gcc gat gat gcg gtg gtg ccc tat atc gcc ctg gcc gcc cgc   1073
86  Phe Tyr Ala Asp Asp Ala Val Val Pro Tyr Ile Ala Leu Ala Ala Arg
87                    80                    85                    90
89  ggg ccg tgg gtg gtc agc ctg aag ggc gcg gtg ctg tat gac gcc ggc   1121
90  Gly Pro Trp Val Val Ser Leu Lys Gly Ala Val Leu Tyr Asp Ala Gly
91              95                    100                   105
93  ggc tac ggc atg ctc ggc ttc ggc cat acc ccg gcc gat atc ctg gag   1169
94  Gly Tyr Gly Met Leu Gly Phe Gly His Thr Pro Ala Asp Ile Leu Glu
95          110                   115                   120
97  gcg gtc ggc aag ccg cag gtg atg gcc aac atc atg act ccc tcg ctg   1217
98  Ala Val Gly Lys Pro Gln Val Met Ala Asn Ile Met Thr Pro Ser Leu
99          125                   130                   135
101 gcc cag ggc cgc ttc att gcc gca atg cgc cgc gaa atc ggc cat acc   1265
102 Ala Gln Gly Arg Phe Ile Ala Ala Met Arg Arg Glu Ile Gly His Thr
103 140                   145                   150                   155
105 cgc ggc ggc tgc ccg ttc tcg cac ttc atg tgc ctg aac tcc ggc tcc   1313
106 Arg Gly Gly Cys Pro Phe Ser His Phe Met Cys Leu Asn Ser Gly Ser
107                   160                   165                   170
109 gaa gcg gtc ggg ctg gcc gcg cgc atc gcc gac atc aac gcc aag ctg   1361
110 Glu Ala Val Gly Leu Ala Ala Arg Ile Ala Asp Ile Asn Ala Lys Leu
111             175                   180                   185
113 atg acc gac ccg ggc gcc cgg cat gcc ggc gcc acg atc aag cgc gtg   1409
114 Met Thr Asp Pro Gly Ala Arg His Ala Gly Ala Thr Ile Lys Arg Val
115         190                   195                   200
117 gtg atc aag ggc agt ttc cac ggc cgt acc gac cgt ccg gcg ctg tat   1457
118 Val Ile Lys Gly Ser Phe His Gly Arg Thr Asp Arg Pro Ala Leu Tyr
119         205                   210                   215
121 tcc gat tcc acc cgc aag gcc tac gat gcg cat ctg gcc agc tac cgc   1505
122 Ser Asp Ser Thr Arg Lys Ala Tyr Asp Ala His Leu Ala Ser Tyr Arg
123 220                   225                   230                   235
125 gac gag cac agc gtc att gcc atc gcc ccg tat gac cag cag gcc ctg   1553
126 Asp Glu His Ser Val Ile Ala Ile Ala Pro Tyr Asp Gln Gln Ala Leu
127                   240                   245                   250
129 cgc cag gtg ttt gcc gat gcc cag gcc aac cac tgg ttc atc gag gcg   1601
130 Arg Gln Val Phe Ala Asp Ala Gln Ala Asn His Trp Phe Ile Glu Ala
131             255                   260                   265
133 gtg ttc ctg gag ccg gtg atg ggc gaa ggc gac ccg ggc cgt gcg gtg   1649
134 Val Phe Leu Glu Pro Val Met Gly Glu Gly Asp Pro Gly Arg Ala Val
135         270                   275                   280
137 ccg gtg gac ttc tac cgc ctg gcc cgt gag ctg acc cgc gaa cac ggc   1697
138 Pro Val Asp Phe Tyr Arg Leu Ala Arg Glu Leu Thr Arg Glu His Gly
139         285                   290                   295
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141 agc ctg ctg ctg atc gat tcg atc cag gcc gcg ctg cgc gtg cac ggc  1745
142 Ser Leu Leu Leu Ile Asp Ser Ile Gln Ala Ala Leu Arg Val His Gly
143 300             305             310             315
145 acc ctg tcc ttc gtc gac tac ccc ggc cac cag gag ctg gag gca ccg  1793
146 Thr Leu Ser Phe Val Asp Tyr Pro Gly His Gln Glu Leu Glu Ala Pro
147             320             325             330
149 gac atg gag acc tac tcc aag gcc ctg aac ggc gcc cag ttc ccg ctg  1841
150 Asp Met Glu Thr Tyr Ser Lys Ala Leu Asn Gly Ala Gln Phe Pro Leu
151             335             340             345
153 tcg gta gtg gcc gtg acc gag cac gcc gcc gcg ctg tac cgc aag ggc  1889
154 Ser Val Val Ala Val Thr Glu His Ala Ala Ala Leu Tyr Arg Lys Gly
155             350             355             360
157 gtg tac ggc aac acc atg acc acc aac ccg cgg gcg ctg gac gtg gcc  1937
158 Val Tyr Gly Asn Thr Met Thr Thr Asn Pro Arg Ala Leu Asp Val Ala
159             365             370             375
161 tgc gcc acc ctg gca cgc ctg gat gag ccg gtc cgc aac aat atc cgc  1985
162 Cys Ala Thr Leu Ala Arg Leu Asp Glu Pro Val Arg Asn Asn Ile Arg
163 380             385             390             395
165 ctg cgt ggc cag cag gcg atg cag aag ctg gaa gca ttg aag gaa cgg  2033
166 Leu Arg Gly Gln Gln Ala Met Gln Lys Leu Glu Ala Leu Lys Glu Arg
167             400             405             410
169 ctg ggg ggc gcg atc acc aag gtg cag ggc acc ggc ctg ctg ttc tcc  2081
170 Leu Gly Gly Ala Ile Thr Lys Val Gln Gly Thr Gly Leu Leu Phe Ser
171             415             420             425
173 tgc gag ctg gcc ccg cag tac aag tgc tac ggg gcc ggc tcc acc gag  2129
174 Cys Glu Leu Ala Pro Gln Tyr Lys Cys Tyr Gly Ala Gly Ser Thr Glu
175             430             435             440
177 gag tgg ctg cgc atg cac ggg gtc aat gtg atc cac ggc ggc gag aat  2177
178 Glu Trp Leu Arg Met His Gly Val Asn Val Ile His Gly Gly Glu Asn
179             445             450             455
181 tcg ctg cgc ttc acc ccg cac ttc ggc atg gac gag gcc gaa ctg gac  2225
182 Ser Leu Arg Phe Thr Pro His Phe Gly Met Asp Glu Ala Glu Leu Asp
183 460             465             470             475
185 ctg ctg gtg gag atg gtc ggg cgt gcg ctg gtc gaa ggc cca cgc cgg  2273
186 Leu Leu Val Glu Met Val Gly Arg Ala Leu Val Glu Gly Pro Arg Arg
187             480             485             490
189 gcc tga tccgcacccg caggacggaa ggcacgagcc caccgtgagg cgggctcttt gc 2331
190 Ala
192 tgcccggcac cagcggcaac aggccgcgct gtcaccggcc aggcggggcg ccggcagtgg 2391
194 gtttcagccg caggggtccg ccctgccagc gcctgcggcg gggcacaggc ttgcgggcat 2451
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205 <211> LENGTH: 6357
206 <212> TYPE: DNA
207 <213> ORGANISM: Flavobacterium lutescens
209 <220> FEATURE:
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,230

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Input Set : **A:\FUJII Sequence listing.txt**
Output Set: **C:\CRF3\06072001\I762230.raw**

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230 ccgcgcaggg gtggccgagc cggttgaaat agcggcccag cagctgggcc gagaacacct 540
232 cgcccagccc ctgcaccctt tcaagcacct cctcgggcag gccgccgatc accgccagcg 600
234 cttccagcaa cccggccagc ttgtcaaagc gtccatccag ccactgcagc aggtcggcag 660
236 aatcctcgcc cagcagttcg gtggccgctt catggtggcg ctggcgcagg gcctgccagg 720
238 catcacgcca gcgcggctga ccgtgggcgg ccagggtagc cagctcgatc aaggcatcgg 780
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VERIFICATION SUMMARY   DATE: 06/07/2001
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Input Set : **A:\FUJII Sequence listing.txt**
Output Set: **C:\CRF3\06072001\I762230.raw**

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L:591 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:601 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:621 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:652 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
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No.	Doccode	Number of pages
1	CRFL	6

Total number of pages: 6

Remarks:

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